

MultiQC

v1.12

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Report generated on 2022-04-23, 15:56 based on data in: /home/khoi1dnyds/RNAseq\_01d/1\_fastqc

📘 Welcome! Not sure where to start?

📺 Watch a tutorial video (6:05)

🗑️ don't show again

General Statistics

📄 Copy table

⚙️ Configure Columns

📊 Plot

Showing %A rows and %B columns.

Sample Name	% Dups	% GC	M Seqs
SRR14689340_lymphoblastic	0.2%	49%	12.7
SRR14689341_lymphoblastic	0.2%	47%	13.6
SRR14689344_myeloid	0.1%	48%	13.0
SRR14689345_myeloid	0.1%	49%	13.0

FastQC

FastQC is a quality control tool for high throughput sequence data, written by Simon Andrews at the Babraham Institute in Cambridge.

Sequence Counts

Sequence counts for each sample. Duplicate read counts are an estimate only.

Number of reads

Percentages

FastQC: Sequence Counts

Export Plot

Unique Reads

Duplicate Reads

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Sequence Quality Histograms

2

2

2

2

The mean quality value across each base position in the read.

FastQC: Mean Quality Scores

Export Plot

Y-Limits: 0 100

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Per Sequence Quality Scores

4

4

The number of reads with average quality scores. Shows if a subset of reads has poor quality.

FastQC: Per Sequence Quality Scores

Export Plot

Y-Limits: 0 8000000

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Per Base Sequence Content

4

4

The proportion of each base position for which each of the four normal DNA bases has been called.

Back to overview heatmap

⏮️ Prev

Next ⏭️

SRR14689344\_myeloid

Export Plot

Y-Limits: 0 100

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Per Sequence GC Content

1

3

1

3

The average GC content of reads. Normal random library typically have a roughly normal distribution of GC content.

Percentages

Counts

FastQC: Per Sequence GC Content

Export Plot

Y-Limits: 0 4

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Per Base N Content

4

4

The percentage of base calls at each position for which an 'N' was called.

FastQC: Per Base N Content

Export Plot

Y-Limits: 0 6

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Sequence Length Distribution

4

4

The distribution of fragment sizes (read lengths) found. See the [FastQC help](#)

FastQC: Sequence Length Distribution

Export Plot

Y-Limits: 0 15000000

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Sequence Duplication Levels

4

4

The relative level of duplication found for every sequence.

FastQC: Sequence Duplication Levels

Export Plot

Y-Limits: 0 100%

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Overrepresented sequences

4

4

The total amount of overrepresented sequences found in each library.

4 samples had less than 1% of reads made up of overrepresented sequences

Adapter Content

4

4

The cumulative percentage count of the proportion of your library which has seen each of the adapter sequences at each position.

No samples found with any adapter contamination > 0.1%

Status Checks

IF Sort by highlight

Min: 0

Max: 1

FastQC: Status Checks

Export Plot

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MultiQC v1.12 - Written by Phil Ewels, available on [GitHub](#).  
This report uses [highCharts](#), [jQuery](#), [jQuery UI](#), [Bootstrap](#), [FileSaver.js](#) and [clipboard.js](#).

SciLifeLab